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SEQUENCE LISTING

TECH CENTER 1600/2900

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<120> Chemokine Receptor

<130> 019934-0007210US

<140> US 09/721,495

<141> 2000-11-21

<150> US 60/159,015

<151> 1999-10-12

<150> US 60/159,210

<151> 1999-10-13

<150> US 60/172,979

<151> 1999-12-20

<150> US 60/173,388

<151> 1999-12-28

<150> US 60/186,626

<151> 2000-03-03

<150> US 09/686,019

<151> 2000-10-10

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1147

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1053)

<220>

<223> chemokine receptor CCX CKR

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1 5 10 15

gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc 96
Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
20 25 30

aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc	144
Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu	
35 40 45	
aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca	192
Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala	
50 55 60	
att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc	240
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile	
65 70 75 80	
ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt	288
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe	
85 90 95	
tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc	336
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys	
100 105 110	
aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag	384
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln	
115 120 125	
ttt ctg gct tgt atc agc ata gac aga tat gtg gca gta act aaa gtc	432
Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val	
130 135 140	
ccc agc caa tca gga gtg gga aaa cca tgc tgg atc atc tgt ttc tgt	480
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys	
145 150 155 160	
gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat	528
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr	
165 170 175	
aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta	576
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu	
180 185 190	
gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga	624
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly	
195 200 205	
ttt gta gta ccc ttt ctt att atg ggg gtg tgc tac ttt atc aca gca	672
Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala	
210 215 220	
agg aca ctc atg aag atg cca aac att aaa ata tct cga ccc cta aaa	720
Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys	
225 230 235 240	
gtt ctg ctc aca gtc gtt ata gtt ttc att gtc act caa ctg cct tat	768
Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr	
245 250 255	
aac att gtc aag ttc tgc cga gcc ata gac atc atc tac tcc ctg atc	816
Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile	
260 265 270	

c1
cont

acc agc tgc aac atg agc aaa cgc atg gac atc gcc atc caa gtc aca 864
Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
275 280 285

gaa agc atc gca ctc ttt cac agc tgc ctc aac cca atc ctt tat gtt 912
Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
290 295 300

ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa 960
Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
305 310 315 320

tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt 1008
Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
325 330 335

gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa 1053
Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
340 345 350

aggtaaaact gctctgcctt ttgcttggat acatatgaat gatgctttcc cctcaaataa 1113

aacatctgcc ttattctgaa aaaaaaaaaa aaam 1147

<210> 2
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<212> PRT
<213> Homo sapiens

<220>
<223> chemokine receptor CCX CKR

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Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
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Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
35 40 45
Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
50 55 60
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
65 70 75 80
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe
85 90 95
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
100 105 110
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
115 120 125
Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
130 135 140
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
145 150 155 160
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
165 170 175
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
180 185 190
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
195 200 205

Phe	Val	Val	Pro	Phe	Leu	Ile	Met	Gly	Val	Cys	Tyr	Phe	Ile	Thr	Ala	
210						215					220					
Arg	Thr	Leu	Met	Lys	Met	Pro	Asn	Ile	Lys	Ile	Ser	Arg	Pro	Leu	Lys	
225					230					235					240	
Val	Leu	Leu	Thr	Val	Val	Ile	Val	Phe	Ile	Val	Thr	Gln	Leu	Pro	Tyr	
			245						250					255		
Asn	Ile	Val	Lys	Phe	Cys	Arg	Ala	Ile	Asp	Ile	Ile	Tyr	Ser	Leu	Ile	
		260						265				270				
Thr	Ser	Cys	Asn	Met	Ser	Lys	Arg	Met	Asp	Ile	Ala	Ile	Gln	Val	Thr	
	275						280					285				
Glu	Ser	Ile	Ala	Leu	Phe	His	Ser	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Val	
290						295					300					
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305					310					315					320	
Tyr	Gly	Ser	Trp	Arg	Arg	Gln	Arg	Gln	Ser	Val	Glu	Glu	Phe	Pro	Phe	
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<210> 3
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 <212> DNA
 <213> Homo sapiens

<220>
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 aaagttttcc cccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
 atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
 ctgaatttgg ctgtagcaga tttactcctt ctattcactc tgcccttttg ggctgttaat 300
 gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca 360
 ctaaaacttg tctctggaat gcagtttctg gcttgatca gcatagacag atatgtggca 420
 gtaactaaag tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480
 gtctggatgg ctgccatctt gctgagcata cccagctgg ttttttatac agtaaatgac 540
 aatgttaggt gcattcccat tttccccgc aacttaggaa catcaatgaa agcattgatt 600
 caaatgctag agatctgcat tggatttgta gtaccctttc ttattatggg ggtgtgctac 660
 tttatcacag caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720
 gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag 780
 ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840
 atggacatcg ccatccaagt cacagaaagc atcgcaactt ttcacagctg cctcaaccga 900
 atcctttatg tttttatggg agcatctttc aaaaactacg ttatgaaagt ggccaagaaa 960
 tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggt 1020
 cctacagagc caaccagtac ttttagcatt taaaggtaaa actgctctgc cttttgcttg 1080
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 aaaaaam 1147

<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

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<400> 5
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<210> 6
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<220>
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			20					25					30			
Phe	Thr	Asp	Phe	Tyr	Cys	Glu	Lys	Asn	Asn	Val	Arg	Gln	Phe	Ala	Ser	
		35					40					45				
His	Phe	Leu	Pro	Pro	Leu	Tyr	Trp	Leu	Val	Phe	Ile	Val	Gly	Ala	Leu	
	50					55				60						
Gly	Asn	Ser	Leu	Val	Ile	Leu	Val	Tyr	Trp	Tyr	Cys	Thr	Arg	Val	Lys	
65					70					75					80	
Thr	Met	Thr	Asp	Met	Phe	Leu	Leu	Asn	Leu	Ala	Ile	Ala	Asp	Leu	Leu	
				85					90					95		
Phe	Leu	Val	Thr	Leu	Pro	Phe	Trp	Ala	Ile	Ala	Ala	Ala	Asp	Gln	Trp	
			100					105					110			
Lys	Phe	Gln	Thr	Phe	Met	Cys	Lys	Val	Val	Asn	Ser	Met	Tyr	Lys	Met	
		115					120					125				
Asn	Phe	Tyr	Ser	Cys	Val	Leu	Leu	Ile	Met	Cys	Ile	Ser	Val	Asp	Arg	
	130					135					140					
Tyr	Ile	Ala	Ile	Ala	Gln	Ala	Met	Arg	Ala	His	Thr	Trp	Arg	Glu	Lys	
145					150					155					160	
Arg	Leu	Leu	Tyr	Ser	Lys	Met	Val	Cys	Phe	Thr	Ile	Trp	Val	Leu	Ala	
				165					170					175		
Ala	Ala	Leu	Cys	Ile	Pro	Glu	Ile	Leu	Tyr	Ser	Gln	Ile	Lys	Glu	Glu	
			180					185					190			
Ser	Gly	Ile	Ala	Ile	Cys	Thr	Met	Val	Tyr	Pro	Ser	Asp	Glu	Ser	Thr	
		195					200					205				
Lys	Leu	Lys	Ser	Ala	Val	Leu	Thr	Leu	Lys	Val	Ile	Leu	Gly	Phe	Phe	
	210					215					220					
Leu	Pro	Phe	Val	Val	Met	Ala	Cys	Cys	Tyr	Thr	Ile	Ile	Ile	His	Thr	
225					230					235					240	
Leu	Ile	Gln	Ala	Lys	Lys	Ser	Ser	Lys	His	Lys	Ala	Leu	Lys	Val	Thr	
				245					250					255		
Ile	Thr	Val	Leu	Thr	Val	Phe	Val	Leu	Ser	Gln	Phe	Pro	Tyr	Asn	Cys	
			260					265					270			
Ile	Leu	Leu	Val	Gln	Thr	Ile	Asp	Ala	Tyr	Ala	Met	Phe	Ile	Ser	Asn	
		275					280					285				
Cys	Ala	Val	Ser	Thr	Asn	Ile	Asp	Ile	Cys	Phe	Gln	Val	Thr	Gln	Thr	
	290					295					300					
Ile	Ala	Phe	Phe	His	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Val	Phe	Val	
305					310					315					320	

C¹
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Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys Asn Leu Gly
 325 330 335
 Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg Arg Glu Gly Ser
 340 345 350
 Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser Gly Ala Leu Ser
 355 360 365
 Leu

<210> 7
 <211> 378
 <212> PRT
 <213> Homo sapiens

<220>
 <223> chemokine receptor CCR7

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 Ile Gly Asp Asn Thr Thr Val Asp Tyr Thr Leu Phe Glu Ser Leu Cys
 35 40 45
 Ser Lys Lys Asp Val Arg Asn Phe Lys Ala Trp Phe Leu Pro Ile Met
 50 55 60
 Tyr Ser Ile Ile Cys Phe Val Gly Leu Leu Gly Asn Gly Leu Val Val
 65 70 75 80
 Leu Thr Tyr Ile Tyr Phe Lys Arg Leu Lys Thr Met Thr Asp Thr Tyr
 85 90 95
 Leu Leu Asn Leu Ala Val Ala Asp Ile Leu Phe Leu Leu Thr Leu Pro
 100 105 110
 Phe Trp Ala Tyr Ser Ala Ala Lys Ser Trp Val Phe Gly Val His Phe
 115 120 125
 Cys Lys Leu Ile Phe Ala Ile Tyr Lys Met Ser Phe Phe Ser Gly Met
 130 135 140
 Leu Leu Leu Leu Cys Ile Ser Ile Asp Arg Tyr Val Ala Ile Val Gln
 145 150 155 160
 Ala Val Ser Ala His Arg His Arg Ala Arg Val Leu Leu Ile Ser Lys
 165 170 175
 Leu Ser Cys Val Gly Ser Ala Ile Leu Ala Thr Val Leu Ser Ile Pro
 180 185 190
 Glu Leu Leu Tyr Ser Asp Leu Gln Arg Ser Ser Ser Glu Gln Ala Met
 195 200 205
 Arg Cys Ser Leu Ile Thr Glu His Val Glu Ala Phe Ile Thr Ile Gln
 210 215 220
 Val Ala Gln Met Val Ile Gly Phe Leu Val Pro Leu Leu Ala Met Ser
 225 230 235 240
 Phe Cys Tyr Leu Val Ile Ile Arg Thr Leu Leu Gln Ala Arg Asn Phe
 245 250 255
 Glu Arg Asn Lys Ala Ile Lys Val Ile Ile Ala Val Val Val Phe
 260 265 270
 Ile Val Phe Gln Leu Pro Tyr Asn Gly Val Val Leu Ala Gln Thr Val
 275 280 285
 Ala Asn Phe Asn Ile Thr Ser Ser Thr Cys Glu Leu Ser Lys Gln Leu
 290 295 300
 Asn Ile Ala Tyr Asp Val Thr Tyr Ser Leu Ala Cys Val Arg Cys Cys
 305 310 315 320
 Val Asn Pro Phe Leu Tyr Ala Phe Ile Gly Val Lys Phe Arg Asn Asp
 325 330 335

C1
 Cont.

Ile Phe Lys Leu Phe Lys Asp Leu Gly Cys Leu Ser Gln Glu Gln Leu
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 Arg Gln Trp Ser Ser Cys Arg His Ile Arg Arg Ser Ser Met Ser Val
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 Glu Ala Glu Thr Thr Thr Thr Phe Ser Pro
 370 375

<210> 8
 <211> 374
 <212> PRT
 <213> Homo sapiens

<220>
 <223> chemokine receptor CCR6

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 Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
 35 40 45
 Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
 50 55 60
 Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
 65 70 75 80
 Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
 85 90 95
 Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
 100 105 110
 Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
 115 120 125
 Phe Asn Cys Gly Met Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
 130 135 140
 Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
 145 150 155 160
 Leu Pro Arg Thr Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
 165 170 175
 Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
 180 185 190
 Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
 195 200 205
 Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
 210 215 220
 Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
 225 230 235 240
 Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
 245 250 255
 Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
 260 265 270
 Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
 275 280 285
 Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
 290 295 300
 Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
 305 310 315 320
 Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
 325 330 335
 Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
 340 345 350

C1
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Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn
 355 360 365
 Ala Ser Ser Phe Thr Met
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<210> 9
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> chemokine receptor STRL33

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 35 40 45
 Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser
 50 55 60
 Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe
 65 70 75 80
 Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val
 85 90 95
 Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
 100 105 110
 Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
 115 120 125
 Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
 130 135 140
 Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu
 145 150 155 160
 Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
 165 170 175
 Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
 180 185 190
 Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
 195 200 205
 Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
 210 215 220
 Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe
 225 230 235 240
 Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
 245 250 255
 His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
 260 265 270
 Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
 275 280 285
 Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
 290 295 300
 Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
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 Thr Ser Met Phe Gln Leu
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C1
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 <211> 740
 <212> DNA
 <213> Homo sapiens

<220>
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 of the CCX CKR gene

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 tattaactt atttaaatta aatttataaa taacatcaaa ataaaaaata aatttaattt 120
 aaataaacca agtaatttgc tattttcgtt ttatttcaat ttgtttaga tatactttta 180
 cgattcacaa aattatgtat gtaaagatta taacactatt tattcttttt agttaaaatc 240
 taattaaatt ttcataattt aaaaatcatt ttacataaaa agtcttcaact tttatttagg 300
 atttaaatgat taagaaaatt ctccagggca ttatgtttat tgtcctgttc aaatccaagc 360
 tctttcacac agaattgtac aagcaaagtt tgagtaacta atcttggggg catattccaa 420
 tgtggctccc attaaagcat ttcaaagagt gctagattca ggctcacata tgttacagca 480
 acaggctata ctctagggaa agaacaaaac agcttgatag aaactgtgtg cttttaagca 540
 tatttagaca aatatctatc ctgtattctc ttggccatct agattggagc catggctttg 600
 gaacagaacc gtcaacagat tattattatg aggagaagtg aaatgaatgg cctgatgact 660
 acagtcagta tgaactgatc tgttcagaga agagacagag gatatgcaca gggttgctcc 720
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<210> 11
 <211> 347
 <212> DNA
 <213> Homo sapiens

<220>
 <223> positions 1-347 of CXC CKR

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 aaagtttttc tccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
 atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
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<210> 12
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:peptide
 translation of non-coding region of SEQ ID NO:1

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<210> 13
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide
translation of non-coding region of SEQ ID NO:1

<400> 13
Cys Phe Pro Leu Lys
1 5

<210> 14
<211> 11
<212> PRT
<213> Artificial Sequence

C1
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<220>
<223> Description of Artificial Sequence:peptide
translation of non-coding region of SEQ ID NO:1

<400> 14
Asn Ile Cys Leu Ile Leu Lys Lys Lys Lys Lys
1 5 10
